

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Withdrawn) A method for comparing a query peptide to a plurality of database peptides comprising the steps of:
 - (a) constructing an index table, said index table comprising a plurality of records corresponding to a plurality of allowed mass values, said records comprising zero or more fields, said constructing step comprising the steps of:
 - (i) selecting a first peptide from said plurality of database peptides;
 - (ii) calculating a plurality of associated masses for said first peptide;
 - (iii) selecting a first associated mass from said plurality of associated masses;
 - (iv) referencing a first record from said plurality of records, said first record corresponding to said first associated mass;
 - (v) entering a first field into said first record, said first field comprising a first peptide index referencing said first peptide;
 - (vi) repeating steps (iii)-(v) for at least one other associated mass from said plurality of associated masses;
 - (vii) repeating steps (i)-(vi) for at least one other peptide from said plurality of database peptides; and
 - (b) generating a plurality of comparison scores, said plurality of comparison scores corresponding to said plurality of database peptides, said generating step comprising the steps of:
 - (i) generating a plurality of query mass values for said query peptide;
 - (ii) selecting a first query mass value from said plurality of query mass values;
 - (iii) referencing a second record from said plurality of records, said second record corresponding to said first query mass value;
 - (iv) selecting a second field from said second record, said second field comprising a second peptide index;

- (v) selecting a first comparison score from said plurality of comparison scores, said first comparison score corresponding to said second peptide index;
 - (vi) incrementing said first comparison score;
 - (vii) repeating steps (ii)-(vi) for at least one other query mass value selected from said plurality of query mass values.
- 2. (Withdrawn) The method of claim 1 wherein said generating step (b)(i) comprises the step of performing mass spectroscopy on said query peptide.
- 3. (Withdrawn) The method of claim 2 wherein said mass spectroscopy is performed by a method selected from the set consisting of: Fourier transform ion cyclotron resonance ("FTICR"), quadrupole mass spectroscopy, ion trap mass spectroscopy, and time-of-flight mass spectroscopy.
- 4. (Withdrawn) The method of claim 1 wherein said calculating step (a)(ii) comprises the step of calculating a plurality of associated masses for said first peptide, said plurality of associated masses comprising a plurality of primary masses and a plurality of complementary masses.
- 5. (Withdrawn) The method of claim 1 wherein said generating step (b) further comprises the step of multiplying said first comparison score by a weight value, wherein said weight value is a function of the type of mass value.
- 6. (Withdrawn) The method of claim 5 wherein said type of mass value is selected from the group consisting of: y-ion, b-ion, peak mass, and complementary mass.
- 7. (Withdrawn) A method for comparing a query peptide to a plurality of database peptides comprising the steps of:
 - (a) constructing a first index table, said first index table comprising a first plurality of records corresponding to a plurality of allowed mass values, said records comprising zero or more fields; and

- (b) constructing a second index table, said second index table comprising a second plurality of records corresponding to said plurality of allowed mass values, said records comprising zero or more fields; and
- (c) calculating a plurality weight values, said weight values set according to the predictive value of said first and second index tables.

8. (Currently Amended) A method for peptide modification evaluation comprising the steps of:

identifying a fragmentation spectrum for a sample containing at least one modified query peptide, the at least one modified query peptide having a mass, at least a portion of which is attributable to a modification associated with the at least one modified query peptide, wherein the fragmentation spectrum is obtained by mass spectrometry and at least a portion of the fragmentation spectrum comprises mass/charge ratios associated with fragments of the at least one modified query peptide that are distributed over a spectral range ranging from zero to an unmodified mass associated with the~~comparing a modified~~
query peptide;

~~to a plurality of database peptides comprising the steps of:~~

- ~~(a) — generating a plurality of query mass values for said modified query peptide;~~
- ~~(b) — identifying a set of modified mass values from said plurality of query mass values;~~
- ~~(c) — determining a spectral range for said modified query peptide;~~
- ~~(d) — subdividing~~apportioning ~~said spectral range for the at least one modified query peptide into a plurality divisions representative of mass intervals of the spectral range thereby distributing the mass ratios for the fragments of the at least one modified query peptide over one or more divisions;~~

~~;~~ and

- ~~(e) — performing a plurality of evaluating fragments of the modified query peptide associated with a searches on said plurality of mass intervals postulating that a modification of one or more fragments within the mass interval has occurred and~~

comparing the modified mass ratio for the one or more fragments ~~modified query peptide~~
with mass ratios for fragments associated with known to the plurality of database peptide
fragmentation spectrum adjusted to account for the modification; and

scoring the mass ratio comparisons between the at least one modified peptide versus
those for the known peptides within each interval and identifying known peptides best
matching the at least one modified peptide when taking the mass of the modification into
account.

9. (Currently Amended) The method of claim 8 further comprising the step of determining a
difference mass for the modified query peptide as being the difference between the
molecular weight of the modified query peptide and the molecular weight of the
unmodified query peptide and further excluding from the analysis said fragments
associated with the modified query peptide where the difference mass is not
known ~~modified mass values during the comparison of the modified query peptide to the~~
~~plurality of database peptides.~~
10. (Currently Amended) The method of claim 8 further comprising the step of determining a
difference mass for the modified query peptide as being the difference between the
molecular weight of the modified query peptide and the molecular weight of the
unmodified query peptide and further adjusting mass ratios for fragments associated with
the modified query peptide ~~said modified mass values during the comparison of the~~
~~modified query peptide to the plurality of database peptides~~ prior to the comparison with
fragments associated with known peptide fragmentation spectrum.
11. (Withdrawn) A method for comparing a query peptide to a plurality of database peptides
comprising the step of constructing an index table, said index table comprising a plurality
of records corresponding to a plurality of allowed mass values, said records comprising
zero or more fields, said constructing step comprising the steps of:
 - (i) selecting a first peptide from said plurality of database peptides;
 - (ii) identifying a modification site on said first peptide;

- (iii) applying a modification to said modification site, producing a first modified peptide;
 - (iv) calculating a plurality of associated masses for said first modified peptide;
 - (v) selecting a first associated mass from said plurality of associated masses;
 - (vi) referencing a first record from said plurality of records, said first record corresponding to said first associated mass;
 - (vii) entering a first field into said first record, said first field comprising a first peptide index referencing said first peptide;
 - (viii) repeating steps (v)-(vii) for at least one other associated mass from said plurality of associated masses;
 - (ix) repeating steps (i)-(viii) for at least one other peptide from said plurality of database peptides.
12. (Currently Amended) The method of claim 8 wherein the modified ~~mass value~~ corresponds to query peptide possesses a modification site selected from the group consisting of: a phosphorylation site, an oxidation site, and a substitution site.
13. (Original) The method of claim 12 wherein said phosphorylation site comprises an amino acid selected from the group consisting of: serine, threonine, and tyrosine.
14. (Original) The method of claim 12 wherein said oxidation site comprises an amino acid selected from the group consisting of: cysteine and methionine.
15. (Original) The method of claim 12 wherein said substitution site comprises an amino acid selected from the group consisting of: glutamine, glutamate, asparagine, and aspartate.
16. (Canceled)
17. (Currently Amended) The method of claim 8 wherein ~~a selected comparison between~~ comparing the modified query peptide mass ratio for the one or more fragments of the modified query peptide and the mass ratios for the fragments associated with known peptide fragmentation spectrum plurality of database peptides further identifies modified

~~mass values for fragments of the modified query peptide that reside within the mass interval of the selected comparison.~~

18. (Canceled)

19. (Currently Amended) The method of claim 8 further comprising collectively evaluating the mass ratio comparisons of the between the modified query peptide to the plurality of database peptides to and known peptides to determine the a putative identity of the modified query peptide by determining the closest match between the modified query peptide and the known peptides when taking the mass of the modification into account.